

We claim:

1. A process for preparing amino acids selected from the group of methionine, homoserine and lysine in transgenic organisms, wherein the process comprises the following steps:
 - 5 a) introduction of a nucleic acid sequence which codes for a threonine-degrading protein or lysine-degrading protein or codes for a threonine-degrading protein and lysine-degrading protein, or
 - b) introduction of a nucleic acid sequence which increases threonine degradation or lysine degradation or threonine degradation and lysine degradation in the
 - 10 transgenic organisms, and
 - c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.
2. A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:
 - 15 a) introduction of a nucleic acid sequence which codes for a threonine-degrading protein which comprises the following consensus sequence

H[X]₂G[X]R[X]₁₉D[X]₇K[X]₂₇G, or

HXDGAR[X]₃A[X]₁₅D[X]₄CXSK[X]₄PXGS[X]₃G[X]₇A[X]₄K[X]₂GGGXRXQXG or
 - b) introduction of a nucleic acid sequence which increases threonine degradation in the transgenic organism, and
 - 20 c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.
3. A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:
 - 25 a) introduction of a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or

LG[X]₉LVYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGGXGT

XEE[X]₂E[X]₂TW[X]₂IG[X]₃KP[X]₄N[X]₃FY[X]₁₄F, or

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- b) introduction of a nucleic acid sequence which increases lysine degradation in the transgenic organisms, and
- c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.

5 4. A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein the process comprises the following steps, solved:

- a) introduction of a nucleic acid sequence which codes for a threonine-degrading protein which comprises the following consensus sequence

H[X]₂G[X]R[X]₁₉D[X]₇K[X]₂₇G, or

10 HXDGAR[X]₃A[X]₁₅D[X]₄CXSK[X]₄PXGS[X]₃G[X]₇A[X]₄K[X]₂GGGXRXQG

and introduction of a nucleic acid sequence which codes for a lysine-degrading protein which comprises the following consensus sequence

G[X]₄GIM[X]₄₅M[X]₂RK[X]₂M[X]₁₁GGXG[X]₃E[X]₂E[X]₃W, or

15 LG[X]₉LVYGG[X]₃GIMGXVA[X]₉G[X]₃GXIP[X]₂₄MHXRK[X]₂M[X]₆F[X]₃PGGXGTXEE
[X]₂E[X]₂TW[X]₂G[X]₃KP[X]₄N[X]₃FY[X]₁₄F, or

- b) introduction of a nucleic acid sequence which codes for proteins which increase threonine degradation and lysine degradation in the transgenic organisms, and
- c) expression of a nucleic acid sequence mentioned under (a) or (b) in the transgenic organism.

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5. A process for preparing amino acids in transgenic organisms as claimed in claim 1, wherein there is introduction in process step (a) as set forth in claims 1 to 4 of a nucleic acid sequence which is selected from the group of nucleic acid sequences:

- i) of a nucleic acid sequence having the sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23 or SEQ ID NO: 25;
- ii) of a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24 or SEQ ID NO: 26, and

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- 5 iii) of a derivative of the nucleic acid sequence depicted in SEQ ID NO: 1, SEQ ID NO: 11, SEQ ID NO: 13, SEQ ID NO: 15, SEQ ID NO: 17, SEQ ID NO: 19, SEQ ID NO: 21, SEQ ID NO: 23 or SEQ ID NO: 25, which codes for polypeptides having the amino acid sequence depicted in SEQ ID NO: 2, SEQ ID NO: 12, SEQ ID NO: 14, SEQ ID NO: 16, SEQ ID NO: 18, SEQ ID NO: 20, SEQ ID NO: 22, SEQ ID NO: 24 or SEQ ID NO: 26 and have at least 50% homology at the amino acid level, with a negligible reduction in the biological activity of the polypeptides.
- 10 6. A process for preparing amino acids in transgenic organisms as claimed in claim 1 or 2 or claims 4 and 5, wherein there is introduction in process step (a) of a nucleic acid sequence which is selected from the group of nucleic acid sequences:
- 15 i) of a nucleic acid sequence obtained owing to the degeneracy of the genetic code through back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10;
- 20 ii) of a derivative of the nucleic acid sequence which is obtained by back-translation of the amino acid sequence depicted in SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10 and which has at least 70% homology at the amino acid level with the aforementioned amino acid sequences, with a negligible reduction in the biological activity of the polypeptides.
7. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 6, wherein the transgenic organism is cultivated and harvested after introduction and expression of the nucleic acid.
- 25 8. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 7, wherein the amino acid is isolated from the organism or the culture medium or the organism and the culture medium.
9. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 8, wherein the essential amino acid methionine is involved.
- 30 10. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 9, wherein the transgenic organism is a microorganism or a plant.
11. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 10, wherein the transgenic organism is a microorganism selected from the group of genera *Corynebacterium*, *Brevibacterium*, *Escherichia*, *Bacillus*, *Rhodotorula*,

Hansenula, Schizosaccharomyces, Saccharomyces, Candida, Claviceps or Flavobacterium.

12. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 11, wherein the transgenic organism is a plant selected from the group of crop plants.
- 5 13. A process for preparing amino acids in transgenic organisms as claimed in claim 12, wherein the transgenic organism is a plant selected from the group of peanut, oilseed rape, canola, sunflower, safflower, olive, sesame, hazelnut, almond, avocado, bay, pumpkin, lettuce, flax, soybean, pistachio, borage, corn, wheat, rye, oats, millet, triticale, rice, barley, cassava, potato, sugar beet, feed beet, aubergine, tomato, pea, alfalfa and
10 perennial grasses and feed crops.
14. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 13, wherein the nucleic acid sequence is derived from a eukaryote.
15. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 14, wherein the nucleic acid sequence is derived from the genus Saccharomyces.
- 15 16. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 15, wherein the nucleic acid sequence is for introduction and for expression incorporated into a nucleic acid construct or a vector.
17. A process for preparing amino acids in transgenic organisms as claimed in claims 1 to 16, wherein additionally biosynthesis genes of the amino acid prepared in the process
20 are introduced into the organism.
18. A nucleic acid construct comprising a nucleic acid sequence as set forth in claims 2 to 6, which is functionally linked to one or more regulatory signals.
19. A vector comprising a nucleic acid sequence as set forth in claims 2 to 6 or a nucleic acid construct as set forth in claim 18.
- 25 20. A transgenic prokaryotic or eukaryotic organism comprising at least one nucleic acid sequence as set forth in claims 2 to 6 or at least one nucleic acid construct as set forth in claim 18 or at least one vector as set forth in claim 19.
21. A transgenic prokaryotic or eukaryotic organism as claimed in claim 20, which is a microorganism or a plant.
- 30 22. A transgenic prokaryotic or eukaryotic organism as claimed in claim 21, which is a microorganism of the genus Corynebacterium or Brevibacterium.
23. A transgenic prokaryotic or eukaryotic organism as claimed in claim 21, which is a plant selected from the group of genus of peanut, oilseed rape, canola, sunflower, safflower,

olive, sesame, hazelnut, almond, avocado, bay, pumpkin, lettuce, flax, soybean, pistachio, borage, corn, wheat, rye, oats, millet, triticale, rice, barley, cassava, potato, sugar beet, feed beet, aubergine, tomato, pea, alfalfa and perennial grasses and feed crops.

- 5 24. The use of the transgenic organisms as set forth in claims 20 to 23 or of an amino acid prepared by a process as set forth in claims 1 to 18 for producing an animal or human food, for producing cosmetics or pharmaceuticals.
- 10 25. An amino acid sequence selected from the group of sequences SEQ ID NO: 3, SEQ ID NO: 4, SEQ ID NO: 5, SEQ ID NO: 6, SEQ ID NO: 7, SEQ ID NO: 8, SEQ ID NO: 9 or SEQ ID NO: 10.